ExPASy Proteomics Server

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Databases   Tools   Services   Mirrors   About   Contact

You are here: ExPASy CA > Tools > Sequence alignment > SIM

Sim

Click here to view these alignments graphically with the LALNVIEW program (mime-type *chemical/x-alv2*).

Click here to download LALNVIEW (Unix, Mac and PC versions available).
You can also have a look at a sample screen of LALNVIEW and access its documentation.

Results of SIM with:

Sequence 1: GLCM_HUMAN, (536 residues)
Sequence 2: seq (497 residues)

using the parameters:

Comparison matrix: BLOSUM62
Number of alignments computed: 20
Gap open penalty: 12
Gap extension penalty: 4

■ Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

```
100.0% identity in 497 residues overlap; Score: 2673.0; Gap frequency: 0.0%

GLCM_HUMAN    40  ARPCIPKSFGYSSVVCVCNATYCDSFDPPTFPALGTFSRYESTRSGRRMELSMGPIQANH
seq            1  ARPCIPKSFGYSSVVCVCNATYCDSFDPPTFPALGTFSRYESTRSGRRMELSMGPIQANH
                  ************************************************************

GLCM_HUMAN   100  TGTGLLLTLQPEQKFQKVKGFGGAMTDAAALNILALSPPAQNLLLKSYFSEEGIGYNIIR
seq           61  TGTGLLLTLQPEQKFQKVKGFGGAMTDAAALNILALSPPAQNLLLKSYFSEEGIGYNIIR
                  ************************************************************

GLCM_HUMAN   160  VPMASCDFSIRTYTYADTPDDFQLHNFSLPEEDTKLKIPLIHRALQLAQRPVSLLASPWT
seq          121  VPMASCDFSIRTYTYADTPDDFQLHNFSLPEEDTKLKIPLIHRALQLAQRPVSLLASPWT
                  ************************************************************

GLCM_HUMAN   220  SPTWLKTNGAVNGKGSLKGQPGDIYHQTWARYFVKFLDAYAEHKLQFWAVTAENEPSAGL
seq          181  SPTWLKTNGAVNGKGSLKGQPGDIYHQTWARYFVKFLDAYAEHKLQFWAVTAENEPSAGL
                  ************************************************************

GLCM_HUMAN   280  LSGYPFQCLGFTPEHQRDFIARDLGPTLANSTHHNVRLLMLDDQRLLLPHWAKVVLTDPE
seq          241  LSGYPFQCLGFTPEHQRDFIARDLGPTLANSTHHNVRLLMLDDQRLLLPHWAKVVLTDPE
                  ************************************************************
```

```
GLCM_HUMAN   340 AAKYVHGIAVEWYLDFLAPAKATLGETHRLFPNTMLFASEACVGSKFWEQSVRLGSWDRG
seq          301 AAKYVHGIAVEWYLDFLAPAKATLGETHRLFPNTMLFASEACVGSKFWEQSVRLGSWDRG
                 ************************************************************

GLCM_HUMAN   400 MQYSHSIITNLLYHVVGWTDWNLALNPEGGPNWVRNFVDSPIIVDITKDTFYKQPMFYHL
seq          361 MQYSHSIITNLLYHVVGWTDWNLALNPEGGPNWVRNFVDSPIIVDITKDTFYKQPMFYHL
                 ************************************************************

GLCM_HUMAN   460 GHFSKFIPEGSQRVGLVASQKNDLDAVALMHPDGSAVVVVLNRSSKDVPLTIKDPAVGFL
seq          421 GHFSKFIPEGSQRVGLVASQKNDLDAVALMHPDGSAVVVVLNRSSKDVPLTIKDPAVGFL
                 ************************************************************

GLCM_HUMAN   520 ETISPGYSIETYLWHRQ
seq          481 ETISPGYSIETYLWHRQ
                 *****************
```

31.8% identity in 22 residues overlap; Score: 32.0; Gap frequency: 0.0%

```
GLCM_HUMAN   303 LGPTLANSTHENVRLLMLDDQR
seq           53 MGPIQANHTGTGLLLTLQFEQK
                  **  ** *        *    *
```

31.8% identity in 22 residues overlap; Score: 32.0; Gap frequency: 0.0%

```
GLCM_HUMAN    92 MGPIQANHTGTGLLLTLQFEQK
seq          264 LGPTLANSTHENVRLLMLDDQR
                  **  ** *        *    *
```

40.0% identity in 15 residues overlap; Score: 31.0; Gap frequency: 0.0%

```
GLCM_HUMAN   451 YKQPMFYHLGHFSKF
seq           26 FDPPTFFALGTFSRY
                   *  *  ** **
```

40.0% identity in 15 residues overlap; Score: 31.0; Gap frequency: 0.0%

```
GLCM_HUMAN    65 FDPPTFFALGTFSRY
seq          412 YKQPMFYHLGHFSKF
                   *  *  ** **
```

28.6% identity in 14 residues overlap; Score: 27.0; Gap frequency: 0.0%

```
GLCM_HUMAN   421 NLALNPEGGPNWVR
seq          173 SLLASPWTSPTWLK
```